

## SEQUENCE LISTING

&lt;110&gt; Bertin, John

&lt;120&gt; NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF

&lt;130&gt; 07334-330001

&lt;140&gt; US 09/841,879

&lt;141&gt; 2001-04-24

&lt;150&gt; US 09/728,721

&lt;151&gt; 2000-12-01

&lt;150&gt; US 09/340,620

&lt;151&gt; 1999-06-28

&lt;160&gt; 19

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (89)...(667)

&lt;400&gt; 1

gtcgacccac gcggtccggca gcaggcaggc tgcagcaggc gagcagcagc aagagtaaaa 60  
 ggtgaccgcg gctgcccacc ccagagcc atg ggg cgg gca cga gat gcc atc 112

Met Gly Arg Ala Arg Asp Ala Ile

1

5

ctg gac gct ctt gaa aac ttg tca ggg gat gaa ctc aaa aag ttc aag 160  
 Leu Asp Ala Leu Glu Asn Leu Ser Gly Asp Glu Leu Lys Lys Phe Lys  
 10 15 20

atg aag ctg ctg aca gtg caa ctg cga gaa ggc tat ggg cgc atc cca 208  
 Met Lys Leu Leu Thr Val Gln Leu Arg Glu Gly Tyr Gly Arg Ile Pro  
 25 30 35 40

cgc ggg gcc ctg ctg cag atg gac gcc ata gat ctc act gac aaa ctt 256  
 Arg Gly Ala Leu Leu Gln Met Asp Ala Ile Asp Leu Thr Asp Lys Leu  
 45 50 55

gtc agc tac tat ctg gag tcg tat ggc ttg gag ctc aca atg act gtg 304  
 Val Ser Tyr Tyr Leu Glu Ser Tyr Gly Leu Glu Leu Thr Met Thr Val  
 60 65 70

ctt aga gac atg ggc tta cag gag ctg gct gag cag ctg caa acg act 352  
 Leu Arg Asp Met Gly Leu Gln Glu Leu Ala Glu Gln Leu Gln Thr Thr  
 75 80 85

aaa gaa gag tct gga gct gtg gca gct gca gcc agt gtc cct gct cag 400  
 Lys Glu Glu Ser Gly Ala Val Ala Ala Ala Ala Ser Val Pro Ala Gln  
 90 95 100

agt aca gcc aga aca gga cac ttt gtg gac cag cac agg caa gca ctc 448  
 Ser Thr Ala Arg Thr Gly His Phe Val Asp Gln His Arg Gln Ala Leu  
 105 110 115 120

att gcc agg gtc aca gaa gtg gac gga gtg ctg gat gct ttg cat ggc 496  
 Ile Ala Arg Val Thr Glu Val Asp Gly Val Leu Asp Ala Leu His Gly  
 125 130 135

agt gtg ctg act gaa gga cag tac cag gca gtt cgt gca gag acc acc 544  
 Ser Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu Thr Thr  
 140 145 150

agc caa gac aag atg agg aag ctc ttc agc ttt gtt cca tcc tgg aac 592  
 Ser Gln Asp Lys Met Arg Lys Leu Phe Ser Phe Val Pro Ser Trp Asn  
 155 160 165

ctg acc tgc aag gac tcc ctc ctc cag gcc ttg aag gaa ata cat ccc 640  
 Leu Thr Cys Lys Asp Ser Leu Leu Gln Ala Leu Lys Glu Ile His Pro  
 170 175 180

tac ttg gtg atg gac ctg gag cag agc tgaggatatct tttccagcta 687  
 Tyr Leu Val Met Asp Leu Glu Gln Ser  
 185 190

cattatctag ctctgactt tgtatacaca atttttgaaa aaacaatttg tatttgtgtt 747  
 taataaaaaaa aaaaaaaaaa gggcggccgc 777

<210> 2

<211> 193

<212> PRT

<213> Mus musculus

<400> 2

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 Gly Asp Glu Leu Lys Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu  
 20 25 30  
 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp  
 35 40 45  
 Ala Ile Asp Leu Thr Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr  
 50 55 60  
 Gly Leu Glu Leu Thr Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu  
 65 70 75 80  
 Leu Ala Glu Gln Leu Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala  
 85 90 95  
 Ala Ala Ala Ser Val Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe  
 100 105 110  
 Val Asp Gln His Arg Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp  
 115 120 125  
 Gly Val Leu Asp Ala Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr  
 130 135 140  
 Gln Ala Val Arg Ala Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu  
 145 150 155 160



gcc ggg cag ctg cag gcg gcc acg cac cag ggc tct gga gcc gcg cca 344  
 Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala Pro  
                   85                                  90                                  95

gct ggg atc cag gcc cct cct cag tgc gca gcc aag cca ggc ctg cac 392  
 Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu His  
                   100                                  105                                  110

ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc aca aac gtt 440  
 Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn Val  
                   115                                  120                                  125

gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg gat gag cag 488  
 Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu Gln  
                   130                                  135                                  140                                  145

tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag atg cgg aag 536  
 Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg Lys  
                                   150                                  155                                  160

ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag gac ttg ctc 584  
 Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu Leu  
                                   165                                  170                                  175

ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag gac ctg gag 632  
 Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu Glu  
                   180                                  185                                  190

cgg agc tgaggctcct tcccagcaac actccggtca gccctggca atcccaccaa 688  
 Arg Ser  
                   195

atcatcctga atctgatctt tttatacaca atatacgaaa agccagcttg aa 740

<210> 5

<211> 195

<212> PRT

<213> Homo sapiens

<400> 5

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 Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu  
                   20                                  25                                  30  
 Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp  
                   35                                  40                                  45  
 Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr  
                   50                                  55                                  60  
 Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu  
                   65                                  70                                  75                                  80  
 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala  
                                   85                                  90                                  95  
 Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu  
                   100                                  105                                  110  
 His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn  
                   115                                  120                                  125

Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu  
 130 135 140  
 Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg  
 145 150 155 160  
 Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu  
 165 170 175  
 Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu  
 180 185 190  
 Glu Arg Ser  
 195

<210> 6  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 atggggcgcg cgcgcgacgc catcctggat gcgctggaga acctgaccgc cgaggagctc 60  
 aagaagtcca agctgaagct gctgtcggtg cgcgtgcgcg agggctacgg gcgcatcccg 120  
 cggggcgcgcg tgctgtccat ggacgccttg gacctaccg acaagctggc cagcttctac 180  
 ctggagacct acggcgccga gctcaccgct aacgtgctgc gcgacatggg cctgcaggag 240  
 atggccgggc agctgcaggc ggccaagcca cagggtctcg gagccgcgcc agctgggatc 300  
 caggccccctc ctcatgcggc agccaagcca ggcctgcaact ttatagacca gcaccgggct 360  
 gcgcttatcg cgagggtcac aaacgttgag tggctgctgg atgctctgta cggaaggctc 420  
 ctgacggatg agcagtacca ggcagtgcgg gccgagccca ccaaccaag caagatgcgg 480  
 aagctcttca gtttcacacc agcctggaac tggacctgca aggacttgct cctccaggcc 540  
 ctaagggagt cccagtccta cctggtggag gacctggagc ggagc 585

<210> 7  
 <211> 84  
 <212> PRT  
 <213> Mus musculus

<400> 7  
 Gly His Phe Val Asp Gln His Arg Gln Ala Leu Ile Ala Arg Val Thr  
 1 5 10 15  
 Glu Val Asp Gly Val Leu Asp Ala Leu His Gly Ser Val Leu Thr Glu  
 20 25 30  
 Gly Gln Tyr Gln Ala Val Arg Ala Glu Thr Thr Ser Gln Asp Lys Met  
 35 40 45  
 Arg Lys Leu Phe Ser Phe Val Pro Ser Trp Asn Leu Thr Cys Lys Asp  
 50 55 60  
 Ser Leu Leu Gln Ala Leu Lys Glu Ile His Pro Tyr Leu Val Met Asp  
 65 70 75 80  
 Leu Glu Gln Ser

<210> 8  
 <211> 85  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Gly Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val  
 1 5 10 15  
 Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr  
 20 25 30

Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys  
                   35                  40                  45  
 Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys  
           50                  55                  60  
 Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu  
   65                  70                  75                  80  
 Asp Leu Glu Arg Ser  
                   85

<210> 9  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Met Glu Ala Arg Asp Lys Gln Val Leu Arg Ser Leu Arg Leu Glu Leu  
   1                  5                  10                  15  
 Gly Ala Glu Val Leu Val Glu Gly Leu Val Leu Gln Tyr Leu Tyr Gln  
           20                  25                  30  
 Glu Gly Ile Leu Thr Glu Asn His Ile Gln Glu Ile Asn Ala Gln Thr  
           35                  40                  45  
 Thr Gly Leu Arg Lys Thr Met Leu Leu Leu Asp Ile Leu Pro Ser Arg  
           50                  55                  60  
 Gly Pro Lys Ala Phe Asp Thr Phe Leu Asp Ser Leu Gln Glu Phe Pro  
   65                  70                  75                  80  
 Trp Val Arg Glu Lys Leu Lys Lys Ala Arg Glu Glu Ala Met  
                   85                  90

<210> 10  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg Glu Asp Ile Val Asn Gln  
   1                  5                  10                  15  
 Met Thr Glu Ala Cys Leu Asn Gln Ser Leu Asp Ala Leu Leu Ser Arg  
           20                  25                  30  
 Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu Val Ser Thr Lys Pro Thr  
           35                  40                  45  
 Arg Thr Ser Lys Val Arg Gln Leu Leu Asp Thr Thr Asp Ile Gln Gly  
           50                  55                  60  
 Glu Glu Phe Ala Lys Val Ile Val Gln Lys Leu Lys Asp Asn Lys Gln  
   65                  70                  75                  80  
 Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu  
                   85                  90

<210> 11  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 11  
 Glu Ser His Pro His Ile Gln Leu Leu Lys Ser Asn Arg Glu Leu Leu  
   1                  5                  10                  15  
 Val Thr His Ile Arg Asn Thr Gln Cys Leu Val Asp Asn Leu Leu Lys  
           20                  25                  30

Asn Asp Tyr Phe Ser Ala Glu Asp Ala Glu Ile Val Cys Ala Cys Pro  
           35                  40                  45  
 Thr Gln Pro Asp Lys Val Arg Lys Ile Leu Asp Leu Val Gln Ser Lys  
       50                  55                  60  
 Gly Glu Glu Val Ser Glu Phe Phe Leu Tyr Leu Leu Gln Gln Leu Ala  
       65                  70                  75                  80  
 Asp Ala Tyr Val Asp Leu Arg Pro Trp Leu  
                   85                  90

<210> 12

<211> 95

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<221> VARIANT

<222> 13, 50

<223> Xaa = Any Amino Acid

<400> 12

Ala Glu Ser Gly Ser Glu Ile Ile Asp Gln His Arg Xaa Ala Leu Leu  
   1                  5                  10                  15  
 Ala Arg Val Thr Glu Asp Pro Asp Ser Leu Leu Asp Ala Leu Leu Ser  
           20                  25                  30  
 Arg Asp Leu Ile Ser Glu Glu Asp Tyr Glu Ala Val Glu Ala Glu Thr  
           35                  40                  45  
 Thr Xaa Leu Ser Lys Val Arg Lys Leu Leu Ile Leu Val Gln Ser Lys  
       50                  55                  60  
 Gly Glu Glu Thr Cys Lys Phe Leu Lys Cys Leu Leu Gln Ala Leu Lys  
       65                  70                  75                  80  
 Asp Ser Ala Ala Tyr Leu Gly Leu Asp Pro Glu Val Leu Glu Ser  
                   85                  90                  95

<210> 13

<211> 97

<212> PRT

<213> Homo sapiens

<400> 13

Met Ala Thr Glu Ser Thr Pro Ser Glu Ile Ile Glu Arg Glu Arg Lys  
   1                  5                  10                  15  
 Lys Leu Leu Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr  
           20                  25                  30  
 Leu Thr Ser Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu  
           35                  40                  45  
 Asn Val Thr Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val  
       50                  55                  60  
 Gln Lys Lys Gly Glu Ala Thr Cys Gln His Phe Leu Lys Cys Leu Phe  
       65                  70                  75                  80  
 Ser Thr Phe Pro Gln Leu Ala Ala Ile Cys Gly Leu Arg His Glu Val  
                   85                  90                  95  
 Leu

<210> 14  
 <211> 108  
 <212> PRT  
 <213> Rattus norvegicus

<400> 14  
 Met Ala Ser Glu Gly Ala Ser Ser Glu Ile Ile Glu Lys Gln Arg Thr  
   1                  5                  10                  15  
 Lys Leu Leu Ser Val Leu Gln Gln Asp Pro Asp Ser Ile Leu Asp Thr  
           20                  25                  30  
 Leu Thr Ser Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu  
           35                  40                  45  
 Ala Ile Thr Asp Pro Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Ile  
           50                  55                  60  
 Gln Lys Lys Gly Glu Asp Ser Cys Cys Cys Phe Leu Lys Cys Leu Ser  
   65                  70                  75                  80  
 Asn Ala Phe Pro Gln Ser Ala Ser Thr Leu Gly Leu Lys Gln Glu Val  
                   85                  90                  95  
 Pro Arg Gln Gly Thr Gly Glu Val Val Glu Val Ser  
                   100                  105

<210> 15  
 <211> 85  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus sequence

<221> VARIANT  
 <222> 2, 5, 18, 20, 21, 29, 34, 45-47, 56, 61, 67, 72, 74-75, 84  
 <223> Xaa = Any Amino Acid

<400> 15  
 Gly Xaa His Phe Xaa Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val  
   1                  5                  10                  15  
 Thr Xaa Val Xaa Xaa Val Leu Asp Ala Leu Tyr Gly Xaa Val Leu Thr  
           20                  25                  30  
 Glu Xaa Gln Tyr Gln Ala Val Arg Ala Glu Thr Thr Xaa Xaa Xaa Lys  
           35                  40                  45  
 Met Arg Lys Leu Phe Ser Phe Xaa Pro Ser Trp Asn Xaa Thr Cys Lys  
           50                  55                  60  
 Asp Xaa Leu Leu Gln Ala Leu Xaa Glu Xaa Xaa Pro Tyr Leu Val Glu  
   65                  70                  75                  80  
 Asp Leu Glu Xaa Ser  
                   85

<210> 16  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 16  
 taggacctcg gtaccgcgcg gcgcg

<210> 17  
 <211> 25



<212> DNA  
<213> Homo sapiens

<400> 17  
cgccggcccc taggacctcg gtacc

25

<210> 18  
<211> 777  
<212> DNA  
<213> Mus musculus

<400> 18

cgccggcccc	tttttttttt	ttttttttta	aacacaaata	caaattgttt	tttcaaaaat	60
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aggccatca	ccaagtaggg	atgtatttcc	ttcaaggcct	ggaggaggga	gtccttgag	180
gtcaggttcc	aggatggaac	aaagctgaag	agcttcctca	tcttgtcttg	gctgggtggc	240
tctgcacgaa	ctgcctggta	ctgtccttca	gtcagcacac	tgccatgcaa	agcatccagc	300
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cctgttctgg	ctgtactctg	agcagggaca	ctggctgcag	ctgccacagc	tccagactct	420
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attgtgagct	ccaagccata	cgactccaga	tagtagctga	caagtttgtc	agtgagatct	540
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actgtcagca	gcttcatctt	gaactttttg	agttcatccc	ctgacaagtt	ttcaagagcg	660
tccaggatgg	catctcgtgc	ccgccccatg	gctctggggg	gggcagccgc	ggtcaccttt	720
tactcttgc	gctgtctgcc	tgtgtcagcc	tgcctgtctgc	cggacgcgtg	ggtcgac	777

<210> 19  
<211> 740  
<212> DNA  
<213> Homo sapiens

<400> 19

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attgccaggg	gctgaccgga	gtgttgctgg	gaaggagcct	cagctccgct	ccaggtectc	120
caccaggtag	gactgggact	cccttagggc	ctggaggagc	aagtccttgc	aggtccagtt	180
ccaggctgg	gtgaaactga	agagcttccg	catcttgctt	gggttggtgg	gctcggcccc	240
cactgcctgg	tactgctcat	ccgtcaggac	cttcccgtac	agagcatcca	gcagccactc	300
aacgtttgtg	accctcgcga	taagcgcagc	ccggtgctgg	tctataaagt	gcaggcctgg	360
cttggctgcc	gactgaggag	gggcctggat	cccagctggc	gcggctccag	agccctgggtg	420
cgtggccgcc	tgcagctgcc	cggccatctc	ctgcaggccc	atgtcgcgca	gcacgttagc	480
ggtgagctcg	gcgccgtagg	tctccaggta	gaagctgacc	agcttgctcg	tgaggtccaa	540
ggcgtccatg	gacagcagcg	cgccccgcgg	gatgcgcccc	tagccctcgc	gcagcggcac	600
cgacagcagc	ttcagcttga	acttcttgag	ctcctcggcg	gtcaggttct	ccagcgcac	660
caggatggcg	tcgcgcgcgc	gccccatggc	tccaggatcc	ccggccgctg	ccgcccgtca	720
ccccgctgca	gccggacgcg					740